

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Luyten, Frank P.
Hoang, Bang
Moos, Jr., Malcolm
Wang, Shouwen

(ii) TITLE OF THE INVENTION: METHOD OF MODULATING TISSUE GROWTH USING
PRZB PROTEIN

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson & Bear
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(C) CITY: Newport Beach
(D) STATE: CA
(E) COUNTRY: U.S.A.
(F) ZIP: 92660

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bartfeld, Neil S
(B) REGISTRATION NUMBER: 39,901
(C) REFERENCE/DOCKET NUMBER: NIH133.001CP1

(ix) TELECOMMUNICATION INFORMATION:

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10023051.12901

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 256...1230
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATAGATGCC	GCGGCCCCAG	AAGTCTTAGA	CGTCGGGAAA	GAGCAGCCGG	AGAGGCAGGG	60
GCGGCGGCGG	CTGGCGCTCG	GCGCAGCTTT	TGGGACCCCA	TTGAGGGAAT	TTGATCCAAG	120
GAAGCTGTGA	GATTGCCGGG	GGAGGAGAAG	CTCCCATATC	ATTGTGTCCA	CTTCCAGGGC	180
GGGGAGGAGG	AAACGGCGGA	GCGGGCCTCT	CGGCGTTCTC	CGCACTGCTG	CACCCTGCCC	240
CATCCTGCCG	AGATC	ATG	GTC	TGC	GGG	291
	Met	Val	Cys	Gly	Ser	
	1				5	
						10
CCG	GCC	GGG	CTA	CTC	GCC	339
Pro	Ala	Gly	Leu	Leu	Ala	---
	15				20	
GGA	GCG	CGG	GCG	GCC	GCC	387
Gly	Ala	Arg	Ala	Ala	Ala	
	30				35	
TCC	CTG	CCC	TGG	AAC	ATG	435
Ser	Leu	Pro	Trp	Asn	Met	
45				50		
ACC	CAG	GCC	AAC	GCC	ATC	483
Thr	Gln	Ala	Asn	Ala	Ile	
				65		
GGC	ACC	CAC	TGC	AGC	CCG	531
Gly	Thr	His	Cys	Ser	Pro	
			80			
GCG	CCC	ATC	TGC	ACC	ATT	579
Ala	Pro	Ile	Cys	Thr	Ile	
	95				100	
AAG	TCT	GTG	TGC	GAG	CGG	627
Lys	Ser	Val	Cys	Glu	Arg	
	110				115	
AAG	TAC	CGC	CAC	TCG	TGG	675
Lys	Tyr	Arg	His	Ser	Trp	
	125				130	
GTA	TAT	GAC	CGC	GGC	GTG	723
Val	Tyr	Asp	Arg	Gly	Val	
				145		
GAC	GGA	GCC	GAT	TTT	CCT	771
Asp	Gly	Ala	Asp	Phe	Pro	
				160		

GTGCACTGGC	CTGCACTTTA	TCATTTGGAT	TTGTGCTGTT	TAATGCTCAG	TAAAATATGC	2337
TTAATAAAAAG	GAAAAAAAAAA	AAAAAAAAAAA	AAAAAAA			2374

(2) INFORMATION FOR SEO ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(v) FRAGMENT TYPE: internal
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

[illegible]

325

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 208...1182
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGGGCCTGG	GCGGSAGGGG	CGGTGGCTGG	AGCTCGGTAA	AGCTCGTGGG	ACCCCATTTG	60										
GGGAATTTGA	TCCAAGGAAG	CGGTGATTGC	CGGGGGAGGA	GAAGCTCCCA	GATCCTTGTG	120										
TCCACTTGCA	GCGGGGGAGG	CGGAGACGCG	GAGCGGGCCT	TTTGGCGTCC	ACTGCGCGGC	180										
TGCACCCTGC	CCCATCCTGC	CGGGATC	ATG	GTC	TGC	GGC	AGC	CCG	GGA	GGG	ATG	234				
			Met	Val	Cys	Gly	Ser	Pro	Gly	Gly	Met					
			1				5									
CTG	CTG	CTG	CGG	GCC	GGG	CTG	CTT	GCC	CTG	GCT	GCT	CTC	TGC	CTG	CTC	282
Leu	Leu	Leu	Arg	Ala	Gly	Leu	Leu	Ala	Leu	Ala	Ala	Leu	Cys	Leu	Leu	
10					15					20					25	
CGG	GTG	CCC	GGG	GCT	CGG	GCT	GCA	GCC	TGT	GAG	CCC	GTC	CGC	ATC	CCC	330
Arg	Val	Pro	Gly	Ala	Arg	Ala	Ala	Ala	Cys	Glu	Pro	Val	Arg	Ile	Pro	
				30					35					40		
CTG	TGC	AAG	TCC	CTG	CCC	TGG	AAC	ATG	ACT	AAG	ATG	CCC	AAC	CAC	CTG	378
Leu	Cys	Lys	Ser	Leu	Pro	Trp	Asn	Met	Thr	Lys	Met	Pro	Asn	His	Leu	
			45					50					55			
CAC	CAC	AGC	ACT	CAG	GCC	AAC	GCC	ATC	CTG	GCC	ATC	GAG	CAG	TTC	GAA	426
His	His	Ser	Thr	Gln	Ala	Asn	Ala	Ile	Leu	Ala	Ile	Glu	Gln	Phe	Glu	
		60					65					70				
GGT	CTG	CTG	GGC	ACC	CAC	TGC	AGC	CCC	GAT	CTG	CTC	TTC	TTC	CTC	TGT	474
Gly	Leu	Leu	Gly	Thr	His	Cys	Ser	Pro	Asp	Leu	Leu	Phe	Phe	Leu	Cys	
	75					80					85					
GCC	ATG	TAC	GCG	CCC	ATC	TGC	ACC	ATT	GAC	TTT	CAG	CAC	GAG	CCC	ATC	522
Ala	Met	Tyr	Ala	Pro	Ile	Cys	Thr	Ile	Asp	Phe	Gln	His	Glu	Pro	Ile	
90					95					100					105	
AAG	CCC	TGT	AAG	TCT	GTG	TGC	GAG	CGG	GCC	CGG	CAG	GGC	TGT	GAG	CCC	570
Lys	Pro	Cys	Lys	Ser	Val	Cys	Glu	Arg	Ala	Arg	Gln	Gly	Cys	Glu	Pro	
				110					115					120		
ATA	CTC	ATC	AAG	TAC	CGC	CAC	TCG	TGG	CCG	GAG	AAC	CTG	GCC	TGC	GAG	618
Ile	Leu	Ile	Lys	Tyr	Arg	His	Ser	Trp	Pro	Glu	Asn	Leu	Ala	Cys	Glu	
			125					130					135			

GAG	CTG	CCA	GTG	TAC	GAC	AGG	GGC	GTG	TGC	ATC	TCT	CCC	GAG	GCC	ATC	666
Glu	Leu	Pro	Val	Tyr	Asp	Arg	Gly	Val	Cys	Ile	Ser	Pro	Glu	Ala	Ile	
		140					145					150				
GTT	ACT	GCG	GAC	GGA	GCT	GAT	TTT	CCT	ATG	GAT	TCT	AGT	AAC	GGA	AAC	714
Val	Thr	Ala	Asp	Gly	Ala	Asp	Phe	Pro	Met	Asp	Ser	Ser	Asn	Gly	Asn	
		155				160					165					
TGT	AGA	GGG	GCA	AGC	AGT	GAA	CGC	TGT	AAA	TGT	AAG	CCT	ATT	AGA	GCT	762
Cys	Arg	Gly	Ala	Ser	Ser	Glu	Arg	Cys	Lys	Cys	Lys	Pro	Ile	Arg	Ala	
					175					180					185	
ACA	CAG	AAG	ACC	TAT	TTC	CGG	AAC	AAT	TAC	AAC	TAT	GTC	ATT	CGG	GCT	810
Thr	Gln	Lys	Thr	Tyr	Phe	Arg	Asn	Asn	Tyr	Asn	Tyr	Val	Ile	Arg	Ala	
				190					195					200		
AAA	GTT	AAA	GAG	ATA	AAG	ACT	AAG	TGC	CAT	GAT	GTG	ACT	GCA	GTA	GTG	858
Lys	Val	Lys	Glu	Ile	Lys	Thr	Lys	Cys	His	Asp	Val	Thr	Ala	Val	Val	
			205					210					215			
GAG	GTG	AAG	GAG	ATT	CTA	AAG	TCC	TCT	CTG	GTA	AAC	ATT	CCA	CGG	GAC	906
Glu	Val	Lys	Glu	Ile	Leu	Lys	Ser	Ser	Leu	Val	Asn	Ile	Pro	Arg	Asp	
		220					225					230				
ACT	GTC	AAC	CTC	TAT	ACC	AGC	TCT	GGC	TGC	CTC	TGC	CCT	CCA	CTT	AAT	954
Thr	Val	Asn	Leu	Tyr	Thr	Ser	Ser	Gly	Cys	Leu	Cys	Pro	Pro	Leu	Asn	
		235				240					245					
GTT	AAT	GAG	GAA	TAT	ATC	ATC	ATG	GGC	TAT	GAA	GAT	GAG	GAA	CGT	TCC	1002
Val	Asn	Glu	Glu	Tyr	Ile	Ile	Met	Gly	Tyr	Glu	Asp	Glu	Glu	Arg	Ser	
		250			255					260					265	
AGA	TTA	CTC	TTG	GTG	GAA	GGC	TCT	ATA	GCT	GAG	AAG	TGG	AAG	GAT	CGA	1050
Arg	Leu	Leu	Leu	Val	Glu	Gly	Ser	Ile	Ala	Glu	Lys	Trp	Lys	Asp	Arg	
				270					275					280		
CTC	GGT	AAA	AAA	GTT	AAG	CGC	TGG	GAT	ATG	AAG	CTT	CGT	CAT	CTT	GGA	1098
Leu	Gly	Lys	Lys	Val	Lys	Arg	Trp	Asp	Met	Lys	Leu	Arg	His	Leu	Gly	
			285					290					295			
CTC	AGT	AAA	AGT	GAT	TCT	AGC	AAT	AGT	GAT	TCC	ACT	CAG	AGT	CAG	AAG	1146
Leu	Ser	Lys	Ser	Asp	Ser	Ser	Asn	Ser	Asp	Ser	Thr	Gln	Ser	Gln	Lys	
		300					305					310				
TCT	GGC	AGG	AAC	TCG	AAC	CCC	CGG	CAA	GCA	CGC	AAC	TAAATCCCGA	AATACA			1198
Ser	Gly	Arg	Asn	Ser	Asn	Pro	Arg	Gln	Ala	Arg	Asn					
		315				320					325					
AAAAGTAACA	CAGTGGACTT	CCTATTAAGA	CTTACTTGCA	TTGCTGGACT	AGCAAAGGAA											1258
AATTGCACTA	TTGCACATCA	TATTCTATTG	TTTACTATAA	AAATCATGTG	ATAACTGATT											1318
ATTACTTCTG	TTTCTCTTTT	GGTTTCTGCT	TCTCTCTTCT	CTCAACCCCT	TTGTAATGGT											1378
TTGGGGGCAG	ACTCTTAAGT	ATATTGTGAG	TTTCTATTTT	CACTAATCAT	GAGAAAAACT											1438
GTTCTTTTGC	AATAATAATA	AATTAAACAT	GCTGTTAAAA	AAAAAA												1484

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Cys Gly Ser Pro Gly Gly Met Leu Leu Leu Arg Ala Gly Leu
1 5 10 15
Leu Ala Leu Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
20 25 30
Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
35 40 45
Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
50 55 60
Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
65 70 75 80
Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
85 90 95
Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
100 105 110
Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
115 120 125
Ser Trp Pro Glu Asn Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
130 135 140
Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
145 150 155 160
Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
165 170 175
Arg Cys Lys Cys Lys Pro Ile Arg Ala Thr Gln Lys Thr Tyr Phe Arg
180 185 190
Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
195 200 205
Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
210 215 220
Ser Ser Leu Val Asn Ile Pro Arg Asp Thr Val Asn Leu Tyr Thr Ser
225 230 235 240
Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Ile Ile
245 250 255
Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
260 265 270
Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
275 280 285
Trp Asp Met Lys Leu Arg His Leu Gly Leu Ser Lys Ser Asp Ser Ser
290 295 300
Asn Ser Asp Ser Thr Gln Ser Gln Lys Ser Gly Arg Asn Ser Asn Pro
305 310 315 320
Arg Gln Ala Arg Asn
325

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Cys	Gln	Pro	Ile	Ser	Ile	Pro	Leu	Cys	Thr	Asp	Ile	Ala	Tyr	Asn	Gln
1				5					10					15	
Thr	Ile	Met	Pro	Asn	Leu	Leu	Gly	His	Thr	Asn	Gln	Glu	Asp	Ala	Gly
			20					25					30		
Leu	Glu	Val	His	Gln	Phe	Tyr	Pro	Leu	Val	Lys	Val	Gln	Cys	Ser	Ala
		35					40					45			
Glu	Leu	Lys	Phe	Phe	Leu	Cys	Ser	Met	Tyr	Ala	Pro	Val	Cys	Thr	Val
	50					55					60				
Leu	Glu	Gln	Ala	Leu	Pro	Pro	Cys	Arg	Ser	Leu	Cys	Glu	Arg	Ala	Gln
65					70					75					80
Gly	Cys	Glu	Ala	Leu	Met	Asn	Lys	Phe	Gly	Phe	Gln	Trp	Pro	Asp	Thr
				85					90					95	
Leu	Lys	Cys	Glu	Lys	Phe	Pro	Val	His	Gly	Arg	Gly	Glu	Leu	Cys	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Glu	Pro	Ile	Thr	Ile	Ser	Ile	Cys	Lys	Asn	Ile	Pro	Tyr	Asn	Met
1				5					10					15	
Thr	Ile	Met	Pro	Asn	Leu	Ile	Gly	His	Thr	Lys	Gln	Glu	Glu	Ala	Gly
			20					25					30		
Leu	Glu	Val	His	Gln	Phe	Ala	Pro	Leu	Val	Lys	Ile	Gly	Cys	Ser	Asp
		35					40					45			
Asp	Leu	Gln	Leu	Phe	Leu	Cys	Ser	Leu	Tyr	Val	Pro	Val	Cys	Thr	Ile
	50					55				60					
Leu	Glu	Arg	Pro	Ile	Pro	Cys	Arg	Ser	Leu	Cys	Glu	Ser	Ala	Arg	
65					70				75					80	
Val	Cys	Glu	Lys	Leu	Met	Lys	Thr	Tyr	Asn	Phe	Asn	Trp	Pro	Glu	Asn
				85					90					95	
Leu	Glu	Cys	Ser	Lys	Phe	Pro	Val	His	Gly	Gly	Glu	Asp	Leu	Cys	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Pro	Thr	Arg	Lys	Leu	Asp	Ser	Phe	Leu	Leu	Leu	Val	Ile	Pro
1				5					10					15	
Gly	Leu	Val	Leu	Leu	Leu	Leu	Pro	Asn	Ala	Tyr	Cys	Ala	Ser	Cys	Glu
			20					25					30		
Pro	Val	Arg	Ile	Pro	Met	Cys	Lys	Ser	Met	Pro	Trp	Asn	Met	Thr	Lys
		35					40					45			
Met	Pro	Asn	His	Leu	His	His	Ser	Thr	Gln	Ala	Asn	Ala	Ile	Leu	Ala
	50					55					60				
Ile	Glu	Gln	Phe	Glu	Gly	Leu	Leu	Thr	Thr	Glu	Cys	Ser	Gln	Asp	Leu
65					70					75				80	
Leu	Phe	Phe	Leu	Cys	Ala	Met	Tyr	Ala	Pro	Ile	Cys	Thr	Ile	Asp	Phe
				85					90					95	
Gln	His	Glu	Pro	Ile	Lys	Pro	Cys	Lys	Ser	Val	Cys	Glu	Arg	Ala	Arg
			100					105					110		
Ala	Gly	Cys	Glu	Pro	Ile	Leu	Ile	Lys	Tyr	Arg	His	Ile	Trp	Pro	Glu
		115					120					125			
Ser	Leu	Ala	Cys	Glu	Glu	Leu	Pro	Val	Tyr	Asp	Arg	Gly	Val	Cys	Ile
	130					135						140			
Ser	Pro	Glu	Ala	Ile	Val	Thr	Val	Glu	Gln	Gly	Thr	Asp	Ser	Met	Pro
145					150					155				160	
Asp	Phe	Pro	Met	Asp	Ser	Asn	Asn	Gly	Asn	Cys	Gly	Ser	Thr	Ala	Gly
				165					170					175	
Glu	His	Cys	Lys	Cys	Lys	Pro	Met	Lys	Ala	Ser	Gln	Lys	Thr	Tyr	Leu
			180					185					190		
Lys	Asn	Asn	Tyr	Asn	Tyr	Val	Ile	Arg	Ala	Lys	Val	Lys	Glu	Val	Lys
		195					200					205			
Val	Lys	Cys	His	Asp	Ala	Thr	Ala	Ile	Val	Glu	Val	Lys	Glu	Ile	Leu
	210					215					220				
Lys	Ser	Ser	Leu	Val	Asn	Ile	Pro	Lys	Asp	Thr	Val	Ile	Leu	Tyr	Thr
225					230					235				240	
Asn	Ser	Gly	Cys	Leu	Cys	Pro	Gln	Leu	Val	Ala	Asn	Glu	Glu	Tyr	Ile
				245					250					255	
Ile	Met	Gly	Tyr	Glu	Asp	Lys	Glu	Arg	Thr	Arg	Leu	Leu	Leu	Val	Glu
			260					265					270		
Gly	Ser	Leu	Ala	Glu	Lys	Trp	Arg	Asp	Arg	Leu	Ala	Lys	Lys	Val	Lys
		275					280					285			
Arg	Trp	Asp	Gln	Lys	Leu	Arg	Arg	Pro	Arg	Lys	Ser	Lys	Asp	Pro	Val
	290					295					300				
Ala	Pro	Ile	Pro	Asn	Lys	Asn	Ser	Asn	Ser	Arg	Gln	Ala	Arg	Ser	
305					310					315					

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Val	Cys	Gly	Ser	Gly	Gly	Met	Leu	Leu	Leu	Ala	Gly	Leu	Leu	Ala
1				5				10					15		

Leu	Ala	Ala	Leu	Leu	Leu	Arg	Val	Pro	Gly	Ala	Arg	Ala	Ala	Ala	Cys
			20					25					30		
Glu	Pro	Val	Arg	Ile	Pro	Leu	Cys	Lys	Ser	Leu	Pro	Trp	Asn	Met	Thr
		35					40					45			
Lys	Met	Pro	Asn	His	Leu	His	His	Ser	Thr	Gln	Ala	Asn	Ala	Ile	Leu
	50					55					60				
Ala	Ile	Glu	Gln	Phe	Glu	Gly	Leu	Leu	Gly	Thr	His	Cys	Ser	Pro	Asp
65					70					75					80
Leu	Leu	Phe	Phe	Leu	Cys	Ala	Met	Tyr	Ala	Pro	Ile	Cys	Thr	Ile	Asp
				85					90					95	
Phe	Gln	His	Glu	Pro	Ile	Lys	Pro	Cys	Lys	Ser	Val	Cys	Glu	Arg	Ala
			100					105					110		
Arg	Gln	Gly	Cys	Glu	Pro	Ile	Leu	Ile	Lys	Tyr	Arg	His	Ser	Trp	Pro
		115					120					125			
Glu	Ser	Leu	Ala	Cys	Glu	Glu	Leu	Pro	Val	Tyr	Asp	Arg	Gly	Val	Cys
	130					135					140				
Ile	Ser	Pro	Glu	Ala	Ile	Val	Thr	Ala	Asp	Gly	Ala	Asp	Phe	Pro	Met
145					150					155					160
Asp	Ser	Ser	Asn	Gly	Asn	Cys	Arg	Gly	Ala	Ser	Ser	Glu	Arg	Cys	Lys
			165						170					175	
Cys	Lys	Pro	Arg	Ala	Ile	Gln	Lys	Thr	Tyr	Phe	Arg	Asn	Asn	Tyr	Asn
			180					185					190		
Tyr	Val	Ile	Arg	Ala	Lys	Val	Lys	Glu	Ile	Lys	Ile	Lys	Cys	His	Asp
	195						200					205			
Val	Thr	Ala	Val	Val	Glu	Val	Lys	Glu	Ile	Leu	Lys	Ser	Ser	Leu	Val
	210					215					220				
Asn	Ile	Pro	Arg	Asp	Thr	Val	Asn	Leu	Tyr	Thr	Ser	Ser	Gly	Cys	Leu
225					230					235					240
Cys	Pro	Pro	Leu	Asn	Val	Asn	Glu	Glu	Tyr	Ile	Ile	Met	Gly	Tyr	Glu
			245						250					255	
Asp	Glu	Glu	Arg	Ser	Arg	Leu	Leu	Leu	Val	Glu	Gly	Ser	Ile	Ala	Glu
			260					265					270		
Lys	Trp	Lys	Asp	Arg	Leu	Gly	Lys	Lys	Val	Lys	Arg	Trp	Asp	Met	Lys
	275						280					285			
Leu	Arg	His	Leu	Gly	Leu	Ser	Asp	Ser	Ser	Ser	Asp	Ser	Thr	Gln	Ser
	290					295					300				
Gln	Lys	Pro	Gly	Arg	Asn	Ser	Asn	Ser	Arg	Gln	Ala	Arg	Asn		
305					310					315					

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu	Thr	Val	Asn	Leu	Tyr	Thr	Ser	Ala	Gly	Cys	Leu	Cys	Pro	Pro	Leu
1				5					10					15	
Asn	Val	Asn	Glu	Glu	Tyr	Leu	Ile	Met	Gly	Tyr	Glu	Phe	Pro		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GARACHGTSA AYCTBTAYAC N

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

RAAYTCRTAN CCCATNAT

18

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 13...13
- (D) OTHER INFORMATION: Aspartic Acid or Histidin
e

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Xaa Gly Ala Asp
1 5 10 15
Phe Pro Met

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gln Gly Cys Glu Pro Ile Leu Ile Lys
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gln Gly Cys Glu Pro Ile Leu Ile Cys Ala Trp Pro Pro Leu Tyr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Glu Thr Val Asn Leu Tyr Thr Ser Ala Gly Cys Leu Cys Pro Pro Leu
1 5 10 15
Asn Val Asn Glu Glu Tyr Leu Ile Met Gly Tyr Glu
20 25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Thr Val Asn Leu Tyr Thr Ser Ser Gly Cys Leu Cys Pro Pro Leu
1 5 10 15
Asn Val Asn Glu Glu Tyr Leu Ile Met Gly Tyr Glu
20 25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTCTGGCTG CCTGTGTCCT CCACTTAACG

30

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCTCCACTTA ACGTTAATGA GGAGTATCTC

30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGGAACATGA CTAAGATGCC C

21

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATATACTGG CAGCTCCTCG

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTCTTTTGGG AAGCCTTCAT GG

22

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCATCGTGGC ATTTCACTTT CA

22

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTTACTGTGC	CAGTCTTCCC	TGTAACCAGC	GACCTGTATT	CCCCCAAGTA	AGCCTACACA	60
TACAGGTTGG	GCAGAATAAC	AATGTCTCCA	ACAAGGAAAT	TGGACTCATT	CCTGCTACTG	120
GTCATACCTG	GACTGGTGCT	TCTCTTATTA	CCCAATGCTT	ACTGTGCTTC	GTGTGAGCCT	180
GTGCGGATTC	CCATGTGCAA	ATCTATGCCA	TGGAACATGA	CCAAGATGCC	CAACCATCTC	240
CACCACAGCA	CTCAAGCCAA	TGCTATCCTG	GCAATTGAAC	AGTTTGAAGG	TTTGCTGACC	300
ACTGAATGTA	GCCAGGACCT	TTTGTTCTTT	CTGTGTGCCA	TGTATGCCCC	CATTTGTACC	360
ATCGATTTCC	AGCATGAACC	AATTAAGCCT	TGCAAGTCCG	TGTGCGAAAG	GGCCAGGGCC	420
GGCTGTGAGC	CCATTCTCAT	AAAGTACCGG	CACACTTGGC	CAGAGAGCCT	GGCATGTGAA	480
GAGCTGCCCCG	TATATGACAG	AGGAGTCTGC	ATCTCCCCAG	AGGCTATCGT	CACAGTGGAA	540
CAAGGAACAG	ATTCAATGCC	AGACTTCCCC	ATGGATTCAA	ACAATGGAAA	TTGCGGAAGC	600
ACGGCAGGTG	AGCACTGTAA	ATGCAAGCCC	ATGAAGGCTT	CCCAAAAGAC	GTATCTCAAG	660
AATAATTACA	ATTATGTAAT	CAGAGCAAAA	GTGAAAGAGG	TGAAAGTGAA	ATGCCACGAC	720
GCAACAGCAA	TTGTGGAAGT	AAAGGAGATT	CTCAAGTCTT	CCCTAGTGAA	CATTCCTAAA	780
GACACAGTGA	CACTGTACAC	CAACTCAGGC	TGCTTGTGCC	CCCAGCTTGT	TGCCAATGAG	840
GAATACATAA	TTATGGGCTA	TGAAGACAAA	GAGCGTACCA	GGCTTCTACT	AGTGGAAGGA	900
TCCTTGGCCG	AAAAATGGAG	AGATCGTCTT	GCTAAGAAAG	TCAAGCGCTG	GGATCAAAAG	960
CTTCGACGTC	CCAGGAAAAG	CAAAGACCCC	GTGGCTCCAA	TTCCCAACAA	AAACAGCAAT	1020
TCCAGACAAG	CGCGTAGTTA	GACTAACGGA	AAGGTGTATG	GAAACTCTAT	GGACTTTGAA	1080
ACTAAGATTT	GCATTGTTGG	AAGAGCAAAA	AAGAAATTGC	ACTACAGCAC	GTTATATTCT	1140
ATTGTTTACT	ACAAGAAGCT	GGTTTAGTTG	ATTGTAGTTC	TCCTTTCCTT	CTTTTTTTTA	1200
TAACATATAT	GCACGTGTTC	CAGGCAGTTT	ATCAACTTCC	AGTGACAGAG	CAGTGACTGA	1260
ATGTAGCTAA	GAGCCTATCA	TCTGATCACT	A			1291